

C. Saoud

1646 #19

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/469,641B

DATE: 03/27/98
TIME: 14:26:30

INPUT SET: S24473.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: HU, JING-SHAN
6 OLSEN, HENRIK
7 ROSEN, CRAIG G.
8
9 (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING VASCULAR
10 ENDOTHELIAL GROWTH FACTOR 3 POLYPEPTIDES AND METHODS FOR
11 PRODUCING THE POLYPEPTIDES
12
13 (iii) NUMBER OF SEQUENCES: 8
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
17 (B) STREET: 1100 NEW YORK AVE, NW
18 (C) CITY: WASHINGTON
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/469,641
31 (B) FILING DATE: 06-JUN-1995
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: STEFFE, ERIC K.
36 (B) REGISTRATION NUMBER: 36,688
37 (C) REFERENCE/DOCKET NUMBER: 1488.1040000
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-371-2600
41 (B) TELEFAX: 202-371-2540
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47      (A) LENGTH: 666 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: both
50      (D) TOPOLOGY: both
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 1..663
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC      48
63      Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
64          1          5          10          15
65
66      CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG      96
67      Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
68          20          25          30
69
70      AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC      144
71      Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
72          35          40          45
73
74      CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC      192
75      Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
76          50          55          60
77
78      AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC      240
79      Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
80          65          70          75          80
81
82      TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC      288
83      Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
84          85          90          95
85
86      CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG      336
87      Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
88          100          105          110
89
90      ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG      384
91      Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
92          115          120          125
93
94      GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC      432
95      Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
96          130          135          140
97
98      CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA CCC TCC      480
99      Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser

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100	145				150					155					160	
101																
102	CCA	GCT	GAC	ATC	ACC	CAA	TCC	CAC	TCC	AGC	CCC	AGG	CCC	CTC	TGC	CCA
103	Pro	Ala	Asp	Ile	Thr	Gln	Ser	His	Ser	Ser	Pro	Arg	Pro	Leu	Cys	Pro
104					165					170					175	
105																
106	CGC	TGC	ACC	CAG	CAC	CAC	CAG	TGC	CCT	GAC	CCC	CGG	ACC	TGC	CGC	TGC
107	Arg	Cys	Thr	Gln	His	His	Gln	Cys	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys
108				180					185					190		
109																
110	CGC	TGT	CGA	CGC	CGC	AGC	TTC	CTC	CGT	TGT	CAA	GGG	CGG	GGC	TTA	GAG
111	Arg	Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu
112			195					200					205			
113																
114	CTC	AAC	CCA	GAC	ACC	TGC	AGG	TGC	CGG	AAG	CTG	CGA	AGG	TGA		
115	Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg			
116		210					215				220					
117																
118																
119	(2) INFORMATION FOR SEQ ID NO:2:															
120																
121																
122																
123																
124																
125																
126																
127																
128																
129																
130	Met	Arg	Arg	Cys	Arg	Ile	Ser	Gly	Arg	Pro	Pro	Ala	Pro	Pro	Gly	Val
131	1				5					10					15	
132																
133	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln	Arg
134				20					25					30		
135																
136	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln	Pro
137			35					40					45			
138																
139	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val	Ala
140		50					55					60				
141																
142	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys
143	65					70					75				80	
144																
145	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val
146					85					90					95	
147																
148	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu
149				100					105					110		
150																
151	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys
152			115					120					125			

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153
154 Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
155 130 135 140
156
157 Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser
158 145 150 155 160
159
160 Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
161 165 170 175
162
163 Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
164 180 185 190
165
166 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
167 195 200 205
168
169 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
170 210 215 220
171
172

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCATGGATCC CAGCCTGATG CCCCTGGCC

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATTCTAGA CCCTGCTGAG TCTGAAAAGC

30

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206
207 (2) INFORMATION FOR SEQ ID NO:5:
208
209 (i) SEQUENCE CHARACTERISTICS:
210 (A) LENGTH: 29 base pairs
211 (B) TYPE: nucleic acid
212 (C) STRANDEDNESS: both
213 (D) TOPOLOGY: linear
214
215 (ii) MOLECULE TYPE: cDNA
216
217
218
219
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
221
222 GACTGCATGC ACCAGAGGAA AGTGGTGTG 29
223
224 (2) INFORMATION FOR SEQ ID NO:6:
225
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 29 base pairs
228 (B) TYPE: nucleic acid
229 (C) STRANDEDNESS: both
230 (D) TOPOLOGY: linear
231
232 (ii) MOLECULE TYPE: cDNA
233
234
235
236
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
238
239 GACTAGATCT CCTTCGCAGC TTCCGGCAC 29
240
241 (2) INFORMATION FOR SEQ ID NO:7:
242
243 (i) SEQUENCE CHARACTERISTICS:
244 (A) LENGTH: 14 amino acids
245 (B) TYPE: amino acid
246 (C) STRANDEDNESS: single
247 (D) TOPOLOGY: Not Relevant
248
249 (ii) MOLECULE TYPE: peptide
250
251
252
253
254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
255
256 Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn
257 1 5 10
258

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SEQUENCE VERIFICATION REPORT
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